RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/549,506
Source: IFW
Date Processed by STIC: 11/16/06

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IFWP

RAW SEQUENCE LISTING DATE: 11/16/2006
PATENT APPLICATION: **US/10/549,506** TIME: 11:03:32

Input Set : **A:\0272wo310.ST25.txt**
Output Set: **N:\CRF4\11162006\J549506.raw**

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  3 <110> APPLICANT: Maxygen ApS
  4       Maxygen Holdings Ltd.
  5       Haaning, Jesper Mortensen
  6       Andersen, Kim Vilbour
  7       Roepke, Mads
  8       Glazer, Steven
 10 <120> TITLE OF INVENTION: FVII or FVIIa Variants
 12 <130> FILE REFERENCE: 0272wo310
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/549,506
C--> 14 <141> CURRENT FILING DATE: 2005-09-16
 14 <150> PRIOR APPLICATION NUMBER: US 60/456,547
 15 <151> PRIOR FILING DATE: 2003-03-20
 17 <150> PRIOR APPLICATION NUMBER: US 60/479,708
 18 <151> PRIOR FILING DATE: 2003-06-19
 20 <160> NUMBER OF SEQ ID NOS: 19
 22 <170> SOFTWARE: PatentIn version 3.2
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1338
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (115)..(1338)
 34 <400> SEQUENCE: 1
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 37 gccgtcttcg tcacccagga ggaagcccat ggcgtcctgc atcgccggcg ccgg gcc      117
 38                                                            Ala
 39                                                            1
 41 aat gcc ttt ctg gaa gag ctc cgc cct ggc tcc ctg gaa cgc gaa tgc      165
 42 Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys
 43             5                  10                  15
 45 aaa gag gaa cag tgc agc ttt gag gaa gcc cgg gag att ttc aaa gac      213
 46 Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp
 47         20                  25                  30
 49 gct gag cgg acc aaa ctg ttt tgg att agc tat agc gat ggc gat cag      261
 50 Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln
 51     35                  40                  45
 53 tgc gcc tcc agc cct tgc cag aac ggg ggc tcc tgc aaa gac cag ctg      309
 54 Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu
 55 50                  55                  60                  65
 57 cag agc tat atc tgc ttc tgc ctg cct gcc ttt gag ggg cgc aat tgc      357
 58 Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys
 59                 70                  75                  80
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61 gaa acc cat aag gat gac cag ctg att tgc gtc aac gaa aac ggg ggc      405
62 Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly Gly
63             85                  90                  95
65 tgc gag cag tac tgc agc gat cac acg ggc acg aag cgg agc tgc cgc      453
66 Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys Arg
67         100                 105                 110
69 tgc cac gaa ggc tat agc ctc ctg gct gac ggg gtg tcc tgc acg ccc      501
70 Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro
71     115                 120                 125
73 acg gtg gaa tac cct tgc ggg aag att ccc att cta gaa aag cgg aac      549
74 Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn
75 130                 135                 140                 145
77 gct agc aaa ccc cag ggc cgg atc gtc ggc ggg aag gtc tgc cct aag      597
78 Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys
79                 150                 155                 160
81 ggg gag tgc ccc tgg cag gtc ctg ctc ctg gtc aac ggg gcc cag ctg      645
82 Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln Leu
83             165                 170                 175
85 tgc ggc ggg acc ctc atc aat acc att tgg gtc gtg tcc gcc gct cac      693
86 Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala His
87         180                 185                 190
89 tgc ttc gat aag att aag aat tgg cgg aac ctc atc gct gtg ctc ggc      741
90 Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly
91     195                 200                 205
93 gaa cac gat ctg tcc gag cat gac ggg gac gaa cag tcc cgc cgg gtg      789
94 Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val
95 210                 215                 220                 225
97 gct cag gtc atc att ccc tcc acc tat gtg cct ggc acg acc aat cac      837
98 Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His
99                 230                 235                 240
101 gat atc gct ctg ctc cgc ctc cac cag ccc gtc gtg ctc acc gat cac      885
102 Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His
103             245                 250                 255
105 gtc gtg cct ctg tgc ctg cct gag cgg acc ttt agc gaa cgc acg ctg      933
106 Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu
107         260                 265                 270
109 gct ttc gtc cgc ttt agc ctc gtg tcc ggc tgg ggc cag ctg ctc gac      981
110 Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu Asp
111     275                 280                 285
113 cgg ggc gct acc gct ctc gag ctg atg gtg ctc aac gtc ccc cgg ctg     1029
114 Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg Leu
115 290                 295                 300                 305
117 atg acc cag gac tgc ctg cag cag tcc cgc aaa gtg ggg gac tcc ccc     1077
118 Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser Pro
119                 310                 315                 320
121 aat atc acg gag tat atg ttt tgc gct ggc tat agc gat ggc tcc aag     1125
122 Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser Lys
123             325                 330                 335
125 gat agc tgc aag ggg gac tcc ggc ggg ccc cat gcc acg cac tat cgc     1173
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126 Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg
127         340                 345                 350
129 ggg acc tgg tac ctc acc ggg atc gtc agc tgg ggc cag ggc tgc gcc     1221
130 Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala
131     355                 360                 365
133 acg gtg ggg cac ttt ggc gtc tac acg cgc gtc agc cag tac att gag     1269
134 Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu
135 370                 375                 380                 385
137 tgg ctg cag aag ctc atg cgg agc gaa ccc cgg ccc ggg gtg ctc ctg     1317
138 Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu Leu
139                 390                 395                 400
141 cgg gcc cct ttc cct tga taa                                       1338
142 Arg Ala Pro Phe Pro
143             405
146 <210> SEQ ID NO: 2
147 <211> LENGTH: 406
148 <212> TYPE: PRT
149 <213> ORGANISM: Homo sapiens
151 <400> SEQUENCE: 2
153 Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu
154 1               5                   10                  15
157 Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys
158             20                  25                  30
161 Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp
162         35                  40                  45
165 Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
166     50                  55                  60
169 Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn
170 65                  70                  75                  80
173 Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
174                 85                  90                  95
177 Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
178             100                 105                 110
181 Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
182         115                 120                 125
185 Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
186     130                 135                 140
189 Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
190 145                 150                 155                 160
193 Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln
194                 165                 170                 175
197 Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala
198             180                 185                 190
201 His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu
202         195                 200                 205
205 Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg
206     210                 215                 220
209 Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
210 225                 230                 235                 240
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Output Set: **N:\CRF4\11162006\J549506.raw**

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213 His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp
214                 245                 250                 255
217 His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
218             260                 265                 270
221 Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
222         275                 280                 285
225 Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
226     290                 295                 300
229 Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
230 305                 310                 315                 320
233 Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
234                 325                 330                 335
237 Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
238             340                 345                 350
241 Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys
242         355                 360                 365
245 Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile
246     370                 375                 380
249 Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu
250 385                 390                 395                 400
253 Leu Arg Ala Pro Phe Pro
254                 405
257 <210> SEQ ID NO: 3
258 <211> LENGTH: 1357
259 <212> TYPE: DNA
260 <213> ORGANISM: Artificial
262 <220> FEATURE:
263 <223> OTHER INFORMATION: Synthetic gene for optimized expression of hFVII
265 <400> SEQUENCE: 3
266 ggatcccgcc accatggtca gccaggccct ccgcctcctg tgcctgctcc tggggctgca     60
268 gggctgcctg gctgccgtct tcgtcaccca ggaggaagcc catggcgtcc tgcatcgccg    120
270 gcgccgggcc aatgcctttc tggaagagct ccgccctggc tccctggaac gcgaatgcaa    180
272 agaggaacag tgcagctttg aggaagcccg ggagattttc aaagacgctg agcggaccaa    240
274 actgttttgg attagctata gcgatggcga tcagtgcgcc tccagccctt gccagaacgg    300
276 gggctcctgc aaagaccagc tgcagagcta tatctgcttc tgcctgcctg cctttgaggg    360
278 gcgcaattgc gaaacccata aggatgacca gctgatttgc gtcaacgaaa acgggggctg    420
280 cgagcagtac tgcagcgatc acacgggcac gaagcggagc tgccgctgcc acgaaggcta    480
282 tagcctcctg gctgacgggg tgtcctgcac gcccacggtg gaataccctt gcgggaagat    540
284 tcccattcta gaaaagcgga acgctagcaa accccagggc cggatcgtcg gcgggaaggt    600
286 ctgccctaag ggggagtgcc cctggcaggt cctgctcctg gtcaacgggg cccagctgtg    660
288 cggcgggacc ctcatcaata ccatttgggt cgtgtccgcc gctcactgct tcgataagat    720
290 taagaattgg cggaacctca tcgctgtgct cggcgaacac gatctgtccg agcatgacgg    780
292 ggacgaacag tcccgccggg tggctcaggt catcattccc tccacctatg tgcctggcac    840
294 gaccaatcac gatatcgctc tgctccgcct ccaccagccc gtcgtgctca ccgatcacgt    900
296 cgtgcctctg tgcctgcctg agcggacctt tagcgaacgc acgctggctt tcgtccgctt    960
298 tagcctcgtg tccggctggg gccagctgct cgaccggggc gctaccgctc tcgagctgat   1020
300 ggtgctcaac gtcccccggc tgatgaccca ggactgcctg cagcagtccc gcaaagtggg   1080
302 ggactccccc aatatcacgg agtatatgtt ttgcgctggc tatagcgatg gctccaagga   1140
304 tagctgcaag ggggactccg gcgggcccca tgccacgcac tatcgcggga cctggtacct   1200
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306 caccgggatc gtcagctggg gccagggctg cgccacggtg gggcactttg gcgtctacac 1260
308 gcgcgtcagc cagtacattg agtggctgca gaagctcatg cggagcgaac cccggcccgg 1320
310 ggtgctcctg cgggcccctt tcccttgata aaagctt 1357
313 <210> SEQ ID NO: 4
314 <211> LENGTH: 31
315 <212> TYPE: DNA
316 <213> ORGANISM: Artificial
318 <220> FEATURE:
319 <223> OTHER INFORMATION: Primer
321 <400> SEQUENCE: 4
322 agctggctag ccactgggca ggtaagtatc a 31
325 <210> SEQ ID NO: 5
326 <211> LENGTH: 31
327 <212> TYPE: DNA
328 <213> ORGANISM: Artificial
330 <220> FEATURE:
331 <223> OTHER INFORMATION: Primer
333 <400> SEQUENCE: 5
334 tggcgggatc cttaagagct gtaattgaac t 31
337 <210> SEQ ID NO: 6
338 <211> LENGTH: 38
339 <212> TYPE: DNA
340 <213> ORGANISM: Artificial
342 <220> FEATURE:
343 <223> OTHER INFORMATION: Primer
345 <400> SEQUENCE: 6
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349 <210> SEQ ID NO: 7
350 <211> LENGTH: 34
351 <212> TYPE: DNA
352 <213> ORGANISM: Artificial
354 <220> FEATURE:
355 <223> OTHER INFORMATION: Primer
357 <400> SEQUENCE: 7
358 ccaattctta atcttgttga agcagtgagc ggcg 34
361 <210> SEQ ID NO: 8
362 <211> LENGTH: 21
363 <212> TYPE: DNA
364 <213> ORGANISM: Artificial
366 <220> FEATURE:
367 <223> OTHER INFORMATION: Primer
369 <400> SEQUENCE: 8
370 ctccgtgata ttgggggagt c 21
373 <210> SEQ ID NO: 9
374 <211> LENGTH: 34
375 <212> TYPE: DNA
376 <213> ORGANISM: Artificial
378 <220> FEATURE:
379 <223> OTHER INFORMATION: Primer

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 11/16/2006
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Input Set : **A:\0272wo310.ST25.txt**
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Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19

VERIFICATION SUMMARY DATE: 11/16/2006
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Input Set : **A:\0272wo310.ST25.txt**
Output Set: **N:\CRF4\11162006\J549506.raw**

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date